# Vladimir Vacic

## List of Publications by Year in descending order



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|---|---|---|---|
| 47 papers | 10,249 citations | 126907 33 h-index | 233421 45 g-index |
| 49 all docs | 49 docs citations | 49 times ranked | 19062 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Genetic overlap analysis of endometriosis and asthma identifies shared loci implicating sex hormones and thyroid signalling pathways. Human Reproduction, 2022, 37, 366-383. | 0.9 | 19 |
| 2 | Genome-wide Study Identifies Association between HLA-Bâˆ—55:01 and Self-Reported Penicillin Allergy. American Journal of Human Genetics, 2020, 107, 612-621. | 6.2 | 34 |
| 3 | Characterization of Prevalence and Health Consequences of Uniparental Disomy in Four Million Individuals from the General Population. American Journal of Human Genetics, 2019, 105, 921-932. | 6.2 | 79 |
| 4 | Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2019, 18, 1091-1102. | 10.2 | 1,414 |
| 5 | 65GENOME-WIDE ANALYSIS OF INSOMNIA AND SLEEP-RELATED TRAITS IN OVER 1 MILLION INDIVIDUALS IDENTIFIES NOVEL GENES AND PATHWAYS. European Neuropsychopharmacology, 2019, 29, S1104-S1105. | 0.7 | 0 |
| 6 | Sequencing and curation strategies for identifying candidate glioblastoma treatments. BMC Medical Genomics, 2019, 12, 56. | 1.5 | 7 |
| 7 | Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways. Nature Genetics, 2019, 51, 394-403. | 21.4 | 593 |
| 8 | Association of Whole-Genome and NETRIN1 Signaling Pathwayâ€“Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2019, 4, 91-100. | 1.5 | 16 |
| 9 | Genome-wide somatic variant calling using localized colored de Bruijn graphs. Communications Biology, 2018, 1, 20. | 4.4 | 85 |
| 10 | A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. Biological Psychiatry, 2018, 83, 1044-1053. | 1.3 | 146 |
| 11 | Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. Lancet Neurology, The, 2017, 16, 898-907. | 10.2 | 191 |
| 12 | Replication and characterization of CADM2 and MSRA genes on human behavior. Heliyon, 2017, 3, e00349. | 3.2 | 80 |
| 13 | Multiethnic GWAS Reveals Polygenic Architecture of Earlobe Attachment. American Journal of Human Genetics, 2017, 101, 913-924. | 6.2 | 29 |
| 14 | Indel variant analysis of short-read sequencing data with Scalpel. Nature Protocols, 2016, 11, 2529-2548. | 12.0 | 99 |
| 15 | Differential burden of rare protein truncating variants in Alzheimerâ€™s disease patients compared to centenarians. Human Molecular Genetics, 2016, 25, ddw150. | 2.9 | 10 |
| 16 | Integrative genetic analysis of mouse and human AML identifies cooperating disease alleles. Journal of Experimental Medicine, 2016, 213, 25-34. | 8.5 | 25 |
| 17 | Genomeâ€wide association study of schizophrenia in Ashkenazi Jews. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 649-659. | 1.7 | 203 |
| 18 | Whole-Exome Sequencing of Metastatic Cancer and Biomarkers of Treatment Response. JAMA Oncology, 2015, 1, 466. | 7.1 | 264 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | The Influence of Microdeletions and Microduplications of 16p11.2 on Global Transcription Profiles. Journal of Child Neurology, 2015, 30, 1947-1953. | 1.4 | 13 |
| 20 | Integrative Analysis of the Mutational Landscape of Mouse and Human AML Identifies Functionally Relevant Leukemia Disease Alleles. Blood, 2015, 126, 1247-1247. | 1.4 | 0 |
| 21 | Comparative sequencing analysis reveals high genomic concordance between matched primary and metastatic colorectal cancer lesions. Genome Biology, 2014, 15, 454. | 8.8 | 296 |
| 22 | Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. Nature Communications, 2014, 5, 3650. | 12.8 | 131 |
| 23 | Detection of a Recurrent DNAJB1-PRKACA Chimeric Transcript in Fibrolamellar Hepatocellular Carcinoma. Science, 2014, 343, 1010-1014. | 12.6 | 388 |
| 24 | Disease variants in genomes of 44 centenarians. Molecular Genetics & Genomic Medicine, 2014, 2, 438-450. | 1.2 | 58 |
| 25 | Genome-wide mapping of IBD segments in an Ashkenazi PD cohort identifies associated haplotypes. Human Molecular Genetics, 2014, 23, 4693-4702. | 2.9 | 49 |
| 26 | Fall risk and gait in Parkinson's disease: The role of the LRRK2 G2019S mutation. Movement Disorders, 2013, 28, 1683-1690. | 3.9 | 82 |
| 27 | The Variance of Identity-by-Descent Sharing in the Wrightâ€“Fisher Model. Genetics, 2013, 193, 911-928. | 2.9 | 38 |
| 28 | Disease-Associated Mutations Disrupt Functionally Important Regions of Intrinsic Protein Disorder. PLoS Computational Biology, 2012, 8, e1002709. | 3.2 | 123 |
| 29 | Disease mutations in disordered regionsâ€”exception to the rule?. Molecular BioSystems, 2012, 8, 27-32. | 2.9 | 93 |
| 30 | High Frequencies of De Novo CNVs in Bipolar Disorder and Schizophrenia. Neuron, 2011, 72, 951-963. | 8.1 | 290 |
| 31 | Duplications of the neuropeptide receptor gene VIPR2 confer significant risk for schizophrenia. Nature, 2011, 471, 499-503. | 27.8 | 296 |
| 32 | Identification, analysis, and prediction of protein ubiquitination sites. Proteins: Structure, Function and Bioinformatics, 2010, 78, 365-380. | 2.6 | 513 |
| 33 | Graphlet Kernels for Prediction of Functional Residues in Protein Structures. Journal of Computational Biology, 2010, 17, 55-72. | 1.6 | 44 |
| 34 | Immune profile and mitotic index of metastatic melanoma lesions enhance clinical staging in predicting patient survival. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20429-20434. | 7.1 | 327 |
| 35 | Microduplications of 16p11.2 are associated with schizophrenia. Nature Genetics, 2009, 41, 1223-1227. | 21.4 | 646 |
| 36 | Small RNAs and the regulation of cis-natural antisense transcripts in Arabidopsis. BMC Molecular Biology, 2008, 9, 6. | 3.0 | 120 |

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|---|---|---|---|
| 37 | The unfoldomics decade: an update on intrinsically disordered proteins. BMC Genomics, 2008, 9, S1. | 2.8 | 485 |
| 38 | A probabilistic method for small RNA flowgram matching. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 75-86. | 0.7 | 10 |
| 39 | MSOAR: A High-Throughput Ortholog Assignment System Based on Genome Rearrangement. Journal of Computational Biology, 2007, 14, 1160-1175. | 1.6 | 67 |
| 40 | DisProt: the Database of Disordered Proteins. Nucleic Acids Research, 2007, 35, D786-D793. | 14.5 | 711 |
| 41 | Characterization of Molecular Recognition Features, MoRFs, and Their Binding Partners. Journal of Proteome Research, 2007, 6, 2351-2366. | 3.7 | 433 |
| 42 | Composition Profiler: a tool for discovery and visualization of amino acid composition differences. BMC Bioinformatics, 2007, 8, 211. | 2.6 | 350 |
| 43 | A PROBABILISTIC METHOD FOR SMALL RNA FLOWGRAM MATCHING. , 2007, , . | | 2 |
| 44 | Analysis of Molecular Recognition Features (MoRFs). Journal of Molecular Biology, 2006, 362, 1043-1059. | 4.2 | 672 |
| 45 | Two Sample Logo: a graphical representation of the differences between two sets of sequence alignments. Bioinformatics, 2006, 22, 1536-1537. | 4.1 | 468 |
| 46 | A Parsimony Approach to Genome-Wide Ortholog Assignment. Lecture Notes in Computer Science, 2006, , 578-594. | 1.3 | 11 |
| 47 | DisProt: a database of protein disorder. Bioinformatics, 2005, 21, 137-140. | 4.1 | 231 |